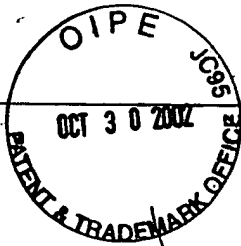


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SEQUENCE LISTING

E1 (1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: EUROSCREEN S.A.  
(B) STREET: Avenue des Becassines 7  
(C) CITY: BRUXELLES  
(E) COUNTRY: BELGIUM  
(F) POSTAL CODE (ZIP): 1160

(A) NAME: COMMUNI DIDIER  
(B) STREET: Groendallaan 19  
(C) CITY: VILVOORDE  
(E) COUNTRY: BELGIUM  
(F) POSTAL CODE (ZIP): 1800

(A) NAME: PIROTTON SABINE  
(B) STREET: Avenue Marius Renard 27a  
(C) CITY: BRUXELLES  
(E) COUNTRY: BELGIUM  
(F) POSTAL CODE (ZIP): 1070

(A) NAME: PARMENTIER MARC  
(B) STREET: Chaussées d'Uccle 304  
(C) CITY: LINKEBEEK  
(E) COUNTRY: BELGIUM

(F) POSTAL CODE (ZIP): 1604

(A) NAME: BOEYNAEMS JEAN-MARIE

(B) STREET: Avenue Peter Benoit 5

(C) CITY: WEMMEL

(E) COUNTRY: BELGIUM

(F) POSTAL CODE (ZIP): 1780

(ii) TITLE OF INVENTION: RECEPTOR AND NUCLEIC ACID MOLECULE ENCODING  
SAID RECEPTOR

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: WO PCT/BE 96/00123

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1429 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:181..1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AAGGGAGCTT GGGTAGGGGC CAGGCTAGCC TGAGTGCACC CAGATGCGCT TCTGTCAGCT 60

CTCCCTAGTG CTTCAACCAC TGCTCTCCCT GCTCTACTTT TTTTGCTCCA GCTCAGGGAT 120

GGGGGTGGGC AGGGAAATCC TGCCACCCTC ACTTCTCCCC TTCCCATCTC CAGGGGGGCC 180

ATG GCC AGT ACA GAG TCC TCC CTG TTG AGA TCC CTA GGC CTC AGC CCA 228

Met Ala Ser Thr Glu Ser Ser Leu Leu Arg Ser Leu Gly Leu Ser Pro

1 5 10 15

GGT CCT GGC AGC AGT GAG GTG GAG CTG GAC TGT TGG TTT GAT GAG GAT 276

Gly Pro Gly Ser Ser Glu Val Glu Leu Asp Cys Trp Phe Asp Glu Asp

20 25 30

TTC AAG TTC ATC CTG CTG CCT GTG AGC TAT GCA GTT GTC TTT GTG CTG 324

Phe Lys Phe Ile Leu Leu Pro Val Ser Tyr Ala Val Val Phe Val Leu

35	40	45	
GGC TTG GGC CTT AAC GCC CCA ACC CTA TGG CTC TTC ATC TTC CGC CTC	372		
Gly Leu Gly Leu Asn Ala Pro Thr Leu Trp Leu Phe Ile Phe Arg Leu			
50	55	60	
CGA CCC TGG GAT GCA ACG GCC ACC TAC ATG TTC CAC CTG GCA TTG TCA	420		
Arg Pro Trp Asp Ala Thr Ala Thr Tyr Met Phe His Leu Ala Leu Ser			
65	70	75	80
GAC ACC TTG TAT GTG CTG TCG CTG CCC ACC CTC ATC TAC TAT TAT GCA	468		
Asp Thr Leu Tyr Val Leu Ser Leu Pro Thr Leu Ile Tyr Tyr Tyr Ala			
85	90	95	
GCC CAC AAC CAC TGG CCC TTT GGC ACT GAG ATC TGC AAG TTC GTC CGC	516		
Ala His Asn His Trp Pro Phe Gly Thr Glu Ile Cys Lys Phe Val Arg			
100	105	110	
TTT CTT TTC TAT TGG AAC CTC TAC TGC ACT GTC CTT TTC CTC ACC TGC	564		
Phe Leu Phe Tyr Trp Asn Leu Tyr Cys Ser Val Leu Phe Leu Thr Cys			
115	120	125	
ATC AGC GTG CAC CGC TAC CTG GGC ATC TGC CAC CCA CTT CGG GCA CTA	612		
Ile Ser Val His Arg Tyr Leu Gly Ile Cys His Pro Leu Arg Ala Leu			
130	135	140	
CGC TGG GGC CGC CCT CGC CTC GCA GGC CTT CTC TGC CTG GCA GTT TGG	660		
Arg Trp Gly Arg Pro Arg Leu Ala Gly Leu Leu Cys Leu Ala Val Trp			

*See  
F1  
cont*

145	150	155	160	
TTG GTC GTA GCC GGC TGC CTC GTG CCC AAC CTG TTC TTT GTC ACA ACC	708			
Leu Val Val Ala Gly Cys Leu Val Pro Asn Leu Phe Phe Val Thr Thr				
165	170	175		
AGC AAC AAA GGG ACC ACC GTC CTG TGC CAT GAC ACC ACT CGG CCT GAA	756			
Ser Asn Lys Gly Thr Thr Val Leu Cys His Asp Thr Thr Arg Pro Glu				
180	185	190		
GAG TTT GAC CAC TAT GTG CAC TTC AGC TCG GCG GTC ATG GGG CTG CTC	804			
Glu Phe Asp His Tyr Val His Phe Ser Ser Ala Val Met Gly Leu Leu				
195	200	205		
TTT GGC GTG CCC TGC CTG GTC ACT CTT GTT TGC TAT GGA CTC ATG GCT	852			
Phe Gly Val Pro Cys Leu Val Thr Leu Val Cys Tyr Gly Leu Met Ala				
210	215	220		
CGT CGC CTG TAT CAG CCC TTG CCA GGC TCT GCA CAG TCG TCT TCT CGC	900			
Arg Arg Leu Tyr Gln Pro Leu Pro Gly Ser Ala Gln Ser Ser Ser Arg				
225	230	235	240	
CTC CGC TCT CTC CGC ACC ATA GCT GTG GTG CTG ACT GTC TTT GCT GTC	948			
Leu Arg Ser Leu Arg Thr Ile Ala Val Val Leu Thr Val Phe Ala Val				
245	250	255		
TGC TTC GTG CCT TTC CAC ATC ACC CGC ACC ATT TAC TAC CTG GCC AGG	996			
Cys Phe Val Pro Phe His Ile Thr Arg Thr Ile Tyr Tyr Leu Ala Arg				

51  
 cont

260 265 270

CTG TTG GAA GCT GAC TGC CGA GTA CTG AAC ATT GTC AAC GTG GTC TAT 1044  
 Leu Leu Glu Ala Asp Cys Arg Val Leu Asn Ile Val Asn Val Val Tyr

275 280 285

AAA GTG ACT CGG CCC CTG GCC AGT GCC AAC AGC TGC CTG GAT CCT GTG 1092  
 Lys Val Thr Arg Pro Leu Ala Ser Ala Asn Ser Cys Leu Asp Pro Val

290 295 300

CTC TAC TTG CTC ACT GGG GAC AAA TAT CGA CGT CAG CTC CGT CAG CTC 1140  
 Leu Tyr Leu Leu Thr Gly Asp Lys Tyr Arg Arg Gln Leu Arg Gln Leu

305 310 315 320

TGT GGT GGT GGC AAG CCC CAG CCC CGC ACG GCT GCC TCT TCC CTG GCA 1188  
 Cys Gly Gly Gly Lys Pro Gln Pro Arg Thr Ala Ala Ser Ser Leu Ala

325 330 335

CTA GTG TCC CTG CCT GAG GAT AGC AGC TGC AGG TGG GCG GCC ACC CCC 1236  
 Leu Val Ser Leu Pro Glu Asp Ser Ser Cys Arg Trp Ala Ala Thr Pro

340 345 350

CAG GAC AGT AGC TGC TCT ACT CCT AGG GCA GAT AGA TTG TAACACGGGA 1285  
 Gln Asp Ser Ser Cys Ser Thr Pro Arg Ala Asp Arg Leu

355 360 365

AGCCGGAAG TGAGAGAAAA GGGGATGAGT GCAGGGCAGA GGTGAGGGAA COCAATAGTG 1345

*See  
 51  
 cont*

ATACCTGGTA AGGTGCTTCT TCCTCTTTTC CAGGCTCTGG AGAGAAGCCC TCACCCTGAG 1405

GGTTGCCACG GAGGCAGGGA TATC 1429

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Ser Thr Glu Ser Ser Leu Leu Arg Ser Leu Gly Leu Ser Pro  
1 5 10 15

Gly Pro Gly Ser Ser Glu Val Glu Leu Asp Cys Trp Phe Asp Glu Asp  
20 25 30

Phe Lys Phe Ile Leu Leu Pro Val Ser Tyr Ala Val Val Phe Val Leu  
35 40 45

Gly Leu Gly Leu Asn Ala Pro Thr Leu Trp Leu Phe Ile Phe Arg Leu  
50 55 60

Arg Pro Trp Asp Ala Thr Ala Thr Tyr Met Phe His Leu Ala Leu Ser

65	70	75	80
Asp Thr Leu Tyr Val Leu Ser Leu Pro Thr Leu Ile Tyr Tyr Tyr Ala			
85	90	95	
Ala His Asn His Trp Pro Phe Gly Thr Glu Ile Cys Lys Phe Val Arg			
100	105	110	
Phe Leu Phe Tyr Trp Asn Leu Tyr Cys Ser Val Leu Phe Leu Thr Cys			
115	120	125	
Ile Ser Val His Arg Tyr Leu Gly Ile Cys His Pro Leu Arg Ala Leu			
130	135	140	
Arg Trp Gly Arg Pro Arg Leu Ala Gly Leu Leu Cys Leu Ala Val Trp			
145	150	155	160
Leu Val Val Ala Gly Cys Leu Val Pro Asn Leu Phe Phe Val Thr Thr			
165	170	175	
Ser Asn Lys Gly Thr Thr Val Leu Cys His Asp Thr Thr Arg Pro Glu			
180	185	190	
Glu Phe Asp His Tyr Val His Phe Ser Ser Ala Val Met Gly Leu Leu			
195	200	205	
Phe Gly Val Pro Cys Leu Val Thr Leu Val Cys Tyr Gly Leu Met Ala			
210	215	220	

*See  
51  
cont*



Arg Arg Leu Tyr Gln Pro Leu Pro Gly Ser Ala Gln Ser Ser Ser Arg

225 230 235 240

Leu Arg Ser Leu Arg Thr Ile Ala Val Val Leu Thr Val Phe Ala Val

245 250 255

Cys Phe Val Pro Phe His Ile Thr Arg Thr Ile Tyr Tyr Leu Ala Arg

260 265 270

Leu Leu Glu Ala Asp Cys Arg Val Leu Asn Ile Val Asn Val Val Tyr

275 280 285

Lys Val Thr Arg Pro Leu Ala Ser Ala Asn Ser Cys Leu Asp Pro Val

290 295 300

Leu Tyr Leu Leu Thr Gly Asp Lys Tyr Arg Arg Gln Leu Arg Gln Leu

305 310 315 320

Cys Gly Gly Gly Lys Pro Gln Pro Arg Thr Ala Ala Ser Ser Leu Ala

325 330 335

Leu Val Ser Leu Pro Glu Asp Ser Ser Cys Arg Trp Ala Ala Thr Pro

340 345 350

Gln Asp Ser Ser Cys Ser Thr Pro Arg Ala Asp Arg Leu

355 360 365

Sub  
31  
cont

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGATCTAGA TACTATGTTC TACACTCTTA CGTGC

35

*See  
fig.  
cont*  
(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

E  
cont

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TCTTAAGCTT GGAGTCACGT ACGAGCAAGC TAGTT

35